IN THE CLAIMS

1-25 (canceled)

26. (currently amended) A method for identifying an intracellular target molecule that binds to a transdominant intracellular bioactive peptide ~~capable of altering~~ that alters the phenotype of a cell, said method comprising the steps:

a) introducing a molecular library comprising different nucleic acid sequences into a plurality of cells, wherein said nucleic acid sequences each comprise a sequence encoding:

i) a candidate randomized ~~bioactive~~ peptide of from 4 to 100 amino acids in length, and wherein said nucleic acid sequences are expressed in said cells to produce a plurality of randomized ~~bioactive~~ peptides;

b) screening said plurality of cells ~~for a cell exhibiting an altered phenotype, wherein said altered phenotype is due to the presence of a transdominant bioactive peptide~~ to detect a peptide that (i) alters the cell phenotype when expressed, and (ii) is transdominant and intracellular;

c) identifying an intracellular target molecule to which said transdominant bioactive ~~agent~~ peptide binds.

27. (currently amended) A method according to claim 26 wherein said identifying comprises:

d) ~~(i)~~ isolating ~~said~~ a cell ~~exhibiting an altered phenotype~~ having an altered phenotype as the result of expression of said transdominant bioactive peptide;

e) ~~(ii)~~ isolating said transdominant bioactive peptide; and

f) ~~(iii)~~ binding said transdominant bioactive agent to ~~said~~ an intracellular target present in said cell to identify said target.

28. (canceled)

29. (currently amended) ~~A method according to claim 26~~ A method for identifying an intracellular target molecule that binds to a transdominant intracellular bioactive peptide that alters the phenotype of a cell, said method comprising the steps:

a) introducing a molecular library comprising different nucleic acid sequences into a plurality of cells, wherein said nucleic acid sequences each comprise a sequence encoding:

i) a candidate transdominant intracellular bioactive peptide of from 4 to 100 amino acids in length, comprising a randomized portion; and ii) ~~wherein said nucleic acids sequences further~~ a presentation structure that presents ~~capable of presenting~~ said randomized bioactive peptides in a

conformationally restricted form wherein a first portion of said presentation structure is joined to the N-terminal end of said candidate transdominant intracellular bioactive peptide, and a second portion of said presentation structure is joined to the C-terminal end of said candidate transdominant intracellular bioactive peptide, and wherein said nucleic acid sequences are expressed in said cells to produce a plurality of randomized peptides;

b) screening said plurality of cells to detect a peptide that (i) alters the cell phenotype when expressed, and (ii) is transdominant and intracellular;

c) identifying an intracellular target molecule to which said transdominant bioactive peptide binds.

30. (canceled)

31. (previously presented) A method according to claim 26 wherein said cells are mammalian cells.

32. (previously presented) A method according to claim 26 wherein said library comprises at least 10^4 different nucleic acids.

33. (previously presented) A method according to claim 26 wherein said library comprises at least 10^5 different nucleic acids.

34. (previously presented) A method according to claim 26 wherein said library comprises at least 10^6 different nucleic acids.

35. (previously presented) A method according to claim 26 wherein said library comprises at least 10^7 different nucleic acids.

36. (previously presented) A method according to claim 26 wherein said library comprises at least 10^8 different nucleic acids.

37. (previously presented) A method according to claim 26 wherein each of said candidate nucleic acids is linked to nucleic acid encoding at least one fusion partner.

39-45 (canceled)